

1	ATGCTGTTCCGCGCCCGGGGCGGTACGGGGCAGGGGCTGGGGGCGGCCGCGAGGCT	60
1	M L F R A R G P V R G R G W G R P A E A	20
61	CCCCGCGCGGGCGCTCGCCGCCCTGGAGCCCCGCCTGGATTGCTGCTGGGCGCTCGCC	120
21	P R R G R S P P W S P A W I C C W A L A	40
121	GGCTGCCAGGCGGCGCTGGGCTGGGGACCTGCCCTCCTCCTCCAGCCGCGCTTCCTCCT	180
41	G C Q A A W A G D L P S S S S R P L P P	60
181	TGCCAGGAGAAAGATTATCACTTTGAATATACGGAATGTGATAGCAGTGGCTCCAGGTGG	240
61	C Q E K D Y H F E Y T E C D S S G S R W	80
241	AGAGTTGCCATTCCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGC	300
81	R V A I P N S A V D C S G L P D P V R G	100
301	AAAGAATGCACTTTCTCCTGTGCTTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGC	360
101	K E C T F S C A S G E Y L E M K N Q V C	120
361	AGTAAGTGTGGTGAAGGCACCTATTCTTGGGCAGTGGCATCAAATTTGATGAATGGGAT	420
121	S K C G E G T Y S L G S G I K F D E W D	140
421	GAATTGCCGGCAGGATTTTCTAACATCGCAACATTCATGGACACTGTGGTGGGCCCTTCT	480
141	E L P A G F S N I A T F M D T V V G P S	160
481	GACAGCAGGCCAGACGGCTGTAACAACCTCTTCTTGGATCCCTCGTGGAACTACATAGAA	540
161	D S R P D G C N N S S W I P R G N Y I E	180
541	TCTAATCGTCATGACTGCACGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC	600
181	S N R D D C T V S L I Y A V H L K K S G	200
601	TATGTCCTCTTTGAGTACCAGTATGTCGACAACAACATCTTCTTTGAGTTCCTTTATTCAA	660
201	Y V F F E Y O Y V D N N I F F E F F I Q	220

FIG. 1A



661	AATGATCAGTGCCAGGAGATGGACACCACCACTGACAAGTGGGTAAAACCTTACAGACAAT	720
221	N D Q C Q E M D T T T D K W V K L T D N	240
721	GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGACA	780
241	G E W G S H S V M L K S G T N I L Y W R	260
781	ACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAAATATCACA	840
261	T T G I L M G S K A V K P V L V K N I T	280
841	ATTGAAGGGGTGGCGTACACATCAGAATGTTTTCTTCAAGCCAGGCACATTCAGCAAC	900
281	I E G V A Y T S E C F P C K P G T F S N	300
901	AAACCAGGTTCACTCAACTGCCAGGTGTGTCCAGAAACACCTATTCTGAGAAAGGAGCC	960
301	K P G S F N C Q V C P R N T Y S E K G A	320
961	AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTTCAGGATCCAGTGAGTGACAGAG	1020
321	K E C I R C K D D S Q F S G S S E C T E	340
1021	CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA	1080
341	R P P C T T K D Y F Q I H T P C D E E G	360
1081	AAGACACAGATAATGTACAACTGGATAGAGCCCAAAATCTGCCGGGAGGATCTCACAGAT	1140
361	K T Q I M Y K W I E P K I C R E D L T D	380
1141	GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGCATTGTCCGCCTTGCAACCCTGGATTT	1200
381	A I R L P P S G E K K D C P P C N P G F	400
1201	TATAACAATGGATCATCTTCTTGCCATCCCTGTCTCCTGGAACATTTTCAGATGGAACC	1260
401	Y N N G S S S C H P C P P G T F S D G T	420
1261	AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG	1320
421	K E C R P C P A G T E P A L G F E Y K W	440

FIG. 1B



1321	TGGAATGTCCTTCCTGGCAACATGAAACTTCCTGCTTCAATGTTGGGAATTCAAAGTGC	1380
441	W N V L P G N M K T S C F N V G N S K C	460
1381	GATGGAATGAATGCTTGGGAGGTGGCTGGACATCATATCCAGAGTGGGGCTGGAGGTTCT	1440
461	D G M N G W E V A G D H I Q S G A G G S	480
1441	GACAAATGATTACCTGATCTTAACTTGCATATCCCAGGATTTAAACCACCAACATCTATG	1500
481	D N D Y L I L N L H I P G F K P P T S M	500
1501	ACTGGAGCCACGGGTTCTGAACTAGGAAGAATAACATTTGTCTTTGAGACCCTCTGTTCA	1560
501	T G A T G S E L G R I T F V F E T L C S	520
1561	GCTGACTGTGTTTTGTACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA	1620
521	A D C V L Y F M V D I N R K S T N V V E	540
1621	TCGTGGGGTGAACCAAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCAACT	1680
541	S W G G T K E K Q A Y T H I I F K N A T	560
1681	TTTACATTTACATGGGCATTCCAGAGAACTAATCAGGTCAGATAATAGACGGTTCATC	1740
561	F T F T W A F Q R T N Q G Q D N R R F I	580
1741	AATGACATGGTGAAGATTTATTCTATCACAGCCACTAATGCAGTTGATGGGGTGGCGTCC	1800
581	N D M V K I Y S I T A T N A V D G V A S	600
1801	TCATGCCGTGCCTGTGCCCTCGGTTCTGAACAGTCGGGTTTCATCGTGTGCCCTGCCCT	1860
601	S C R A C A L G S E Q S G S S C V P C P	620
1861	CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGAAGGAATGTCCACCTGACACCTAC	1920
621	P G H Y I E K E T N Q C K E C P P D T Y	640
1921	CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGTATTCCATGCGGGCCTGGGAGTAAA	1980
641	L S I H Q V Y G K E A C I P C G P G S K	660

FIG. 1C



1981	AACAATCAGGACCATTGGTTTCTATAGTACTGCTTTTCTACCATGAAAAAGAAAAT	2040
661	N N Q D H S V C Y S D C F F Y H E K E N	680
2041	CAGATTTTGCACATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTGAATGGCCCC	2100
681	Q I L H Y D F S N L S S V G S L M N G P	700
2101	AGCTTCACCTCCAAAGGAACAAAATACTTCCATTCTTCAATATCAGTTTATGTGGGCAT	2160
701	S F T S K G T K Y F H F F N I S L C G H	720
2161	GAGGGAAGAAGATGGCTCTCTGTACCAACAATATAACAGACTTTACAGTAAAAGAAATA	2220
721	E G K K M A L C T N N I T D F T V K E I	740
2221	GTGGCAGGTCAGATGATTACACAAATTTGGTAGGGCATTGTATGCCAGTCAACAATT	2280
741	V A G S D D Y T N L V G A F V C Q S T I	760
2281	ATTCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA	2340
761	I P S E S K G F R A A L S S Q S I I L A	780
2341	GATACATTCATAGGAGTCACAGTTGAAACCACATTGAAAAATATTAATATAAAAGAAGAT	2400
781	D T F I G V T V E T T L K N I N I K E D	800
2401	ATGTTCCCAGTTCCAACAAGCCAAATACCAGATGTGCATTTCTTTTATAAGTCTTCTACA	2460
801	M F P V P T S Q I P D V H F F Y K S S T	820
2461	GCAACAACATCTGTATTAATGGCCGATCAACTGCTGTGAAAAATGAGGTGTAATCCTACT	2520
821	A T T S C I N G R S T A V K M R C N P T	840
2521	AAATCTGGAGCAGCAGTGATTTTCACTCCCCAGCAAGTCCCCAGCAGGTACCTGTGATGGG	2580
841	K S G A G V I S V P S K C P A G T C D G	860
2581	TGTACGTTCTATTTCTGTGGGACAGTGCTGAAGCTTGCCCTCTGTGTACGGAGCATGAC	2640
861	C T F Y F L W E S A E A C P L C T E H D	880

FIG. 1D



FIG. 1E



FIG. 2A

		10	20	30		
1		MLPRARGPVRGRGWGRBAHAPRRGRSFFWS				TR16.aa
1	M	-	-	-	-	EMB CAB41042.1 TNFR
1	M	-	-	-	-	emb CAA53576.1 OX40
		40	50	60		
31		PAWICCWALAGCQAAWAGDLSSSSSRPLEP				TR16.aa
10	-	-	-	-	-	EMB CAB41042.1 TNFR
13	-	-	-	-	-	emb CAA53576.1 OX40
		70	80	90		
61		CQEKDYHFEYTECDSSGSRWRVAIPNSAVD				TR16.aa
23	-	-	-	-	-	EMB CAB41042.1 TNFR
26	-	-	-	-	-	emb CAA53576.1 OX40
		100	110	120		
91		CSGLPDEVRGKECTFSCASGEYLEMKNOVC				TR16.aa
30	-	-	-	-	-	EMB CAB41042.1 TNFR
31	-	-	-	-	-	emb CAA53576.1 OX40
		130	140	150		
121		SKCGEGTYSLSGSIKFDDEWDELPAGFSNIA				TR16.aa
51	-	-	-	-	-	EMB CAB41042.1 TNFR
43	-	-	-	-	-	emb CAA53576.1 OX40
		160	170	180		
151		TFMDTVVGPSDSRFDGCNNSSWIPRGNYIE				TR16.aa
51	-	-	-	-	-	EMB CAB41042.1 TNFR
43	-	-	-	-	-	emb CAA53576.1 OX40
		190	200	210		
181		SNRDDCTVSLIYAVBELKKSQGVFFFEYQYVD				TR16.aa
51	-	-	-	-	-	EMB CAB41042.1 TNFR
43	-	-	-	-	-	emb CAA53576.1 OX40
		220	230	240		
211		NNIFFEFPFIQNDQCQEMDTTTRWVKLTDN				TR16.aa
51	-	-	-	-	-	EMB CAB41042.1 TNFR
43	-	-	-	-	-	emb CAA53576.1 OX40
		250	260	270		
241		GEWGSHSVMLKSGTNILYWRTTGILMGSKA				TR16.aa
51	-	-	-	-	-	EMB CAB41042.1 TNFR
43	-	-	-	-	-	emb CAA53576.1 OX40
		280	290	300		
271		VKPVLVKNITIEGVAYTSECFCPKPGTFSN				TR16.aa
51	-	-	-	-	-	EMB CAB41042.1 TNFR
43	-	-	-	-	-	emb CAA53576.1 OX40
		310	320	330		
301		KPGSFNCOVCFRNTYSEKGAKECIRCKDDS				TR16.aa
62	-	-	-	-	-	EMB CAB41042.1 TNFR
54	-	-	-	-	-	emb CAA53576.1 OX40

FIG. 2B

	340	350	360	
331	Q F S G S S E C T E R P E C T T R D Y F Q I H T P C D E E G			TR16.aa
66	-			EMB
58	-			emb
	370	380	390	
361	K T Q I M Y K W I E P R I C R E D I T D A I R L P P S G E K			TR16.aa
66	-			EMB
58	-			emb
	400	410	420	
391	K D C P P C N E G F Y N N G S S S C H P C P P G T F S D G T			TR16.aa
70	T K C E R C P P H T Y T A I P N Y S N G C - - - - -			EMB
62	T V C R P C G P G F Y N D V V S - S K P C - - - - -			emb
	430	440	450	
421	K E C R P C P A G T E R A L G F E Y K W W N V L P G N M R T			TR16.aa
91	H Q C R K C - - P T G S - - - - - F D R V			EMB
82	K P C T W C N L R S G S - - - - - E R K Q			emb
	460	470	480	
451	S C F N V G N S K C D G M N G W E V A G D H I O S G A G G S			TR16.aa
105	K C T G T Q N S K C S C L P G W Y C A T D S S Q T - - - - -			EMB
98	L C T A T Q D T V C R C R A G - - - - - T Q P L D S - - - - -			emb
	490	500	510	
481	D N D Y L I L N L H I P G F K P T S M T G A T G S E L G R			TR16.aa
130	-			EMB
119	-			emb
	520	530	540	
511	I T F V F E T L C S A D C V L Y F M V D I N R K S T N V V E			TR16.aa
132	-			EMB
122	-			emb
	550	560	570	
541	S W G G T K E K Q A Y T H I I F R N A T F T F T W A F O R T			TR16.aa
137	-			EMB
127	-			emb
	580	590	600	
571	N O G O D N R R E I N D M V K I Y S I T A T N A V D G V A S			TR16.aa
137	-			EMB
127	-			emb
	610	620	630	
601	S C R A C A L G S E Q S G S S C V P C P P G H Y I E K E T N			TR16.aa
141	-			EMB
128	-			emb

FIG. 2C

631	QCKECPPDTYLSLHOVYGRKACIPCGPGSK	TR16.aa	
147	-----GGI	EMB	CAB41042.1 TNFR
134	-----SPG	emb	CAA53576.1 OX40
661	NNQDESVCYSDCFFPYHKKENQILLYDFSNL	TR16.aa	
150	DQGNPIC	EMB	CAB41042.1 TNFR
137	DNA	emb	CAA53576.1 OX40
691	SSVGSIMNGESPITSKGTKEFFHFNISLCGH	TR16.aa	
158	-----KS	EMB	CAB41042.1 TNFR
142	-----KPWTN	emb	CAA53576.1 OX40
721	EGKRMALCTNNITDFTVKRIVAGSDDYTNL	TR16.aa	
163	GE-----Y	EMB	CAB41042.1 TNFR
150	AGKH-----TLQPASNSDAI	emb	CAA53576.1 OX40
751	VGAFCOSTIIPSESKGFRAALSSQSILLA	TR16.aa	
166	-----CD	EMB	CAB41042.1 TNFR
166	-----CEDRDPEATQPQETQGP PARPI	emb	CAA53576.1 OX40
781	DTFIGVTVEETTLKNNINIKEDMFVPTSQIP	TR16.aa	
168	-----	EMB	CAB41042.1 TNFR
191	PT-----EAWP-RTSQGP	emb	CAA53576.1 OX40
811	DVHFFYKSSSTATTSKINGRSTAVKMR CNPT	TR16.aa	
168	-----	EMB	CAB41042.1 TNFR
203	-----STRPVEVP GGRAVAAIL	emb	CAA53576.1 OX40
841	KSGAGVISVPSKCBAGTCDGCTFFFLWESA	TR16.aa	
168	-----	EMB	CAB41042.1 TNFR
220	-----GLGLV-----LGLL	emb	CAA53576.1 OX40
871	EACPLCTEHDFFEIEGACKTGFQETLYVWN	TR16.aa	
168	-----YL	EMB	CAB41042.1 TNFR
229	-----GPL-----AILLALLYL	emb	CAA53576.1 OX40
901	EPKWCIGKISLREKKLATCETVDFWLKVGA	TR16.aa	
170	-----RNYRLDP	EMB	CAB41042.1 TNFR
242	-----RDQRLPDAHKP	emb	CAA53576.1 OX40


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961  L E N
184  K C - N
276  K I

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TR16.aa

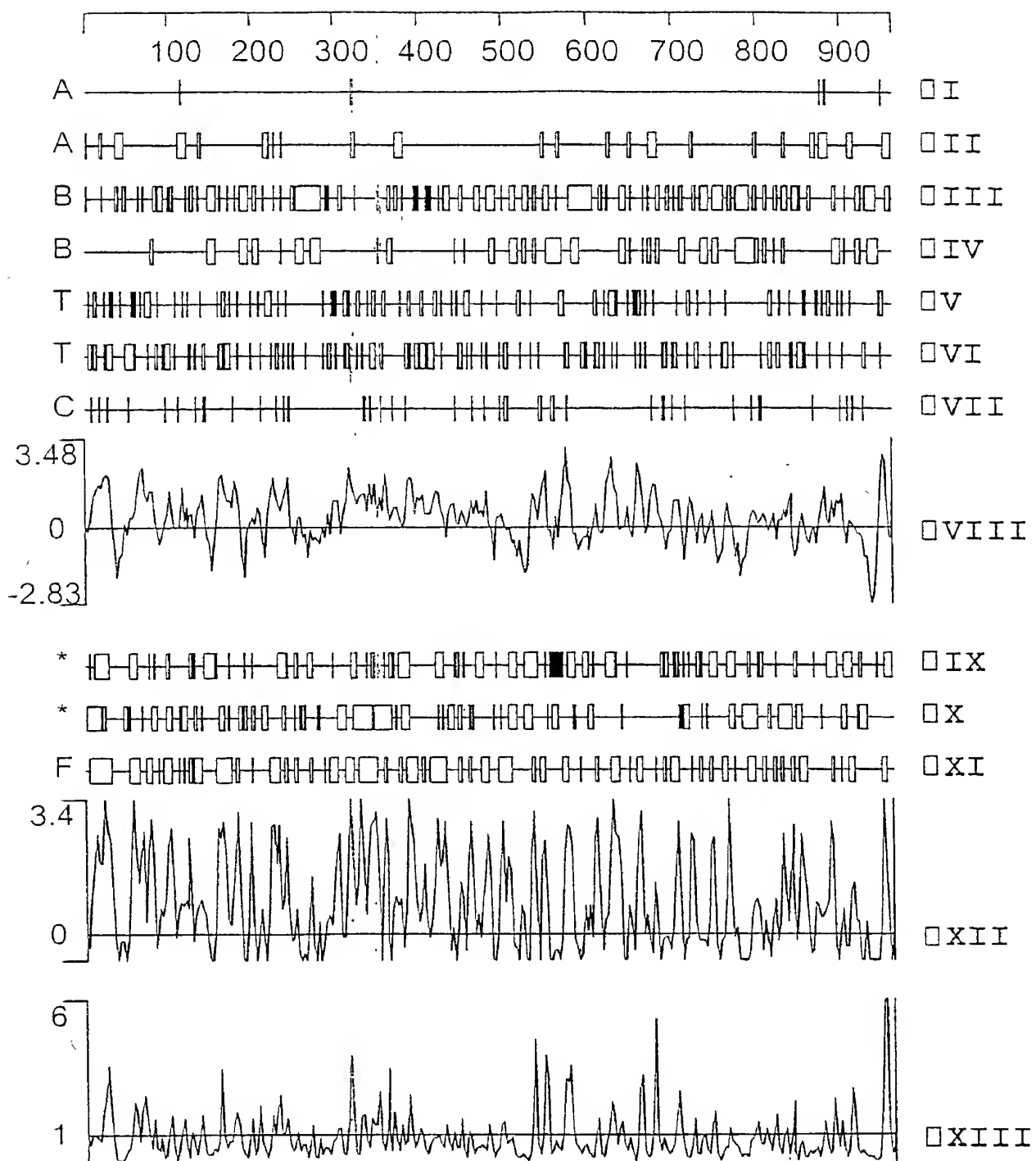


FIG. 3

1 ATGCTGTTCCCGCCCCGGGGCCCGTACGGGGCAGGGGCTGGGGGCGCCGGCGGAGGCT 60
1 M L F R A R G P V R G R G W G R P A E A 20

61 CCCCCCGCGGGCGCTCGCCGCCCTGGAGCCCCGCTGGATTGCTGCTGGGCGCTCCCC 120
21 P R R G R S P P W S P A W I C C W A L A 40

121 GGCTGCCAGGCGGCTGGGCTGGGGACCTGCCCTCCTCCTCCAGCCCGCGCTTCCTCCT 180
41 G C Q A A W A G D L P S S S S R P L P P 60

181 TGCCAGGAGAAAGATTATCACTTTGAATATACCGAATGTGATAGCAGTGGCTCCAGGTGG 240
61 C Q E K D Y H F E Y T E C D S S G S R W 80

241 AGAGTTGCCATTCCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGC 300
81 R V A I P N S A V D C S G L P D P V R G 100

301 AAAGAATGCACTTTCTCCTGTGCTTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGC 360
101 K E C T F S C A S G E Y L E M K N Q V C 120

361 AGTAAGTGTGGTGAAGGCACCTATTCCTTGGGCAGTGGCATCAAATTTGATGAATGGGAT 420
121 S K C G E G T Y S L G S G I K F D E W D 140

421 GAATTGCCGGCAGGATTTTCTAACATCGCAACATTCATGGACACTGTGGTGGGCGCTTCT 480
141 E L P A G F S N I A T F M D T V V G P S 160

481 GACAGCAGGCCAGACGGCTGTAACAACTCTTCTTGATCCCTCGTGGAACTACATAGAA 540
161 D S R P D G C N N S S W I P R G N Y I E 180

541 TCTAATCGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600
181 S N R D D C T V S L I Y A V H L K K S G 200

601 TATGCTTCTTTGAGTACCAGTATGTGACAACAACATCTTCTTTGAGTTCTTTATTCAA 660
201 Y V F F E Y Q Y V D N N I F F E F F I Q 220

661 AATGATCAGTGCCAGGAGATGACACCACCACTGACAAGTGGGTAAACTTACAGACAAT 720
221 N D Q C Q E M D T T T D K W V K L T D N 240

FIG. 4A



721	GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA	780
241	G E W G S H S V M L K S G T N I L Y W R	260
781	ACTACAGGCATCCTTATGGGTCTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAAATATCACA	840
261	T T G I L M G S K A V K P V L V K N I T	280
841	ATTGAAGGGGTGGCGTACACATCAGAATGTTTTCTTGCAGCCAGGCACATTCAGCAAC	900
281	I E G V A Y T S E C F P C K P G T F S N	300
901	AAACCAGGTTCAATCAACTGCCAGGTGTGTCCCAGAAACACCTATTCTGAGAAAGGAGCC	960
301	K P G S F N C Q V C P R N T Y S E K G A	320
961	AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTTCAGGATCCAGTGAGTGACAGAG	1020
321	K E C I R C K D D S Q F S G S S E C T E	340
1021	CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA	1080
341	R P P C T T K D Y F Q I H T P C D E E G	360
1081	AAGACACAGATAATGTACAAGTGGATAGAGCCCCAAATCTGCCGGGAGGATCTCACAGAT	1140
361	K T Q I M Y K W I E P K I C R E D L T D	380
1141	GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGGATTGTCCGCCTTGCAACCCTGGATTT	1200
381	A I R L P P S G E K K D C P P C N P G F	400
1201	TATAACAATGGATCATCTTCTTGCCATCCCTGTCTCTCTGGAACATTTTCAGATGGAACC	1260
401	Y N N G S S S C H P C P P G T F S D G T	420
1261	AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG	1320
421	K E C R P C P A G T E P A L G F E Y K W	440
1321	TGGAATGTCCTTCTGGCAACATGAAAACCTCTGCTTCAATGTTGGGAATTCAAAGTGC	1380
441	W N V L P G N M K T S C F N V G N S K C	460
1381	GATGGAATGAATGGTTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT	1440
461	D G M N G W E V A G D H I O S G A G G S	480

FIG. 4B



1441 GACAATGATTACCTGATCTTAAACTTGCATATCCCAGGATTTAAACCACCAACATCTATG 1500
 481 D N D Y L I L N L H I P G F K P P T S M 500

1501 ACTGGAGCCACGGGTTCTGAACTAGGAAGAATAACATTTGTCTTTGAGACCCTCTGTTCA 1560
 501 T G A T G S E L G R I T F V F E T L C S 520

1561 GCTGACTGTGTTTTGTACTTCATCGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620
 521 A D C V L Y F M V D I N R K S T N V V E 540

1621 TCGTGGGGTGAACCAAAGAAAACAAGCTTACACCCATATCATCTCAAGAATGCAACT 1680
 541 S W G G T K E K Q A Y T H I I F K N A T 560

1681 TTTACATTTACATGGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTTCATC 1740
 561 F T F T W A F Q R T N Q G Q D N R R F I 580

1741 AATGACATGGTGAAGATTTATTCTATCACAGCCACTAATGCAGTTGATGGGGTGGCGTCC 1800
 581 N D M V K I Y S I T A T N A V D G V A S 600

1801 TCATGCCGTGCCTGTGCCCTCGGTTCTGAACAGTCCGGTTCATCGTGTGTCCCCTGCCCT 1860
 601 S C R A C A L G S E Q S G S S C V P C P 620

1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGCAAGGAATGTCCACCTGACACCTAC 1920
 621 P G H Y I E K E T N Q C K E C P P D T Y 640

1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGATTCCATGCGGGCCTGGGAGTAAA 1980
 641 L S I H Q V Y G K E A C I P C G P G S K 660

1981 AACAAATCAGGACCATTGCGTTTGCTATAGTGAAGTCTTTTCTACCATGAAAAAGAAAAT 2040
 661 N N Q D H S V C Y S D C F F Y H E K E N 680

2041 CAGATTTTGCATATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTAAATGAATGGCCCC 2100
 681 Q I L H Y D F S N L S S V G S L M N G P 700

2101 AGCTTCACCTCCAAAGGAACAAAATACTTCCATTTCTTCAATATCAGTTTATGTGGGCAT 2160
 701 S F T S K G T K Y F H F F N I S L C G H 720

FIG. 4C



2161 GAGGGGAAGAAGATGGCTCTCTGTACCAACAATATAACAGACTTTACACTAAAAGAAATA 2220
721 E G K K M A L C T N N I T D F T V K E I 740

2221 GTGGCAGGGTCAGATGATTACACAAATTTGGTAGGGGCATTGTATGCCAGTCAACAATT 2280
741 V A G S D D Y T N L V G A F V C Q S T I 760

2281 ATTCCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA 2340
761 I P S E S K G F R A A L S S Q S I I L A 780

2341 GATACATTCATAGGAGTCACAGTTGAAACCACATTGAAAAATATTAATATAAAAGAAGAT 2400
781 D T F I G V T V E T T L K N I N I K E D 800

2401 ATGTTCCAGTTCCAACAAGCCAAATACCAGATGTGCATTTCTTTTATAAGTCTTCTACA 2460
801 M F P V P T S Q I P D V H F F Y K S S T 820

2461 GCAACAACATCTTGTATTAATGCGGATCAACTGCTGTGAAAAATGAGGTGTAATCCTACT 2520
821 A T T S C I N G R S T A V K M R C N P T 840

2521 AAATCTGGAGCAGGAGTGATTTTCAGTCCCCAGCAAGTCCCCAGCAGGTACCTGTGATGGG 2580
841 K S G A G V I S V P S K C P A G T C D G 860

2581 TGTACGTTCTATTTCTGTGGGAGAGTGCTGAAGCTTGCCCTCTGTGTACCGAGCATGAC 2640
861 C T F Y F L W E S A E A C P L C T E H D 880

2641 TTCCATCAGATTGAGGGAGCCTGCAAGAGAGGATTTTCAGGAAACCTTGATGTGTGGAAT 2700
881 F H E I E G A C K R G F Q E T L Y V W N 900

2701 GAACCTAAATGGTGCAATTAAGGAATTTCTTTGCTGAGAAAAAGTTGGCAACCTGTGAA 2760
901 E P K W C I K G I S L P E K K L A T C E 920

2761 ACGGTTGACTTTTGGCTGAAGGTGGGAGCCGGTGTGGGAGCTTTTACTGCCGTTTGTCTG 2820
921 T V D F W L K V G A G V G A F T A V L L 940

2821 GTGGCTCTGACCTGCTACTTCTGAAAAAGAATCAAAAACTGGAATACAAATATTTCCAAG 2880
941 V A L T C Y F W K K N Q K L E Y K Y S K 960

FIG. 4D



2881 TTAGTAATGACGACTAACTCAAAGAGTGTGAACTCCCGGCTGCAGACAGTTGTGCTATC 2940
 961 L V M T T N S K E C E L P A A D S C A I 980

2941 ATGGAAGGAGAAGATAATGAAGAGGAAGTTGTATATTCCAATAAACAGTCACTACTAGGA 3000
 981 M E G E D N E E E V V Y S N K Q S L L G 1000

3001 AAACCTCAAATCTTTGGCAACCAAGGAAAAAGAAGACCATTTTGAATCTGTTCAACTGAAA 3060
 1001 K L K S L A T K E K E D H F E S V Q L K 1020

3061 ACCTCAAGATCCCCAAATATATGAAGAGACAGTGTGTAGCCTTGAGACTAATGAACAAA 3120
 1021 T S R S P N I * 1028

3121 GAAACCTGCTCTAGTTTTACAGGACCATATTTTAGGGTCTGTCTCATACCTGTCACATT 3180

3181 GGTGATCTCACAGAGGAGGGCCATGCCGCTGAAAAGGAAGGAGATTGAAACATTTGATT 3240

3241 GCCTTATCACATGGTCAAGTACCTTGCCAAATAAAGGAAAGCAAATGATTTGGGTCTCAA 3300

3301 CTGAAGATGAAGCTCAACTCAGGAAGAGATTTATCTGTATATACACATAACTGAAAACCA 3360

3361 AGTTTAAGCCCACCAATGCACTGCTGATGCATGCCATATAATTAATGGGTAACCTTTTATT 3420

3421 CTTTATGATGTCTACATAACAAGTGTGATTTGGAAGGCACATGTGAGCATATGCATTATG 3480

3481 ATCCAATTTATGTTTTTCTTTGTTTATATTTGGGGAAAATTAAAATTTTTTAAGGTA 3540

3541 AAAAAAAAAAAAAA 3556

FIG. 4E



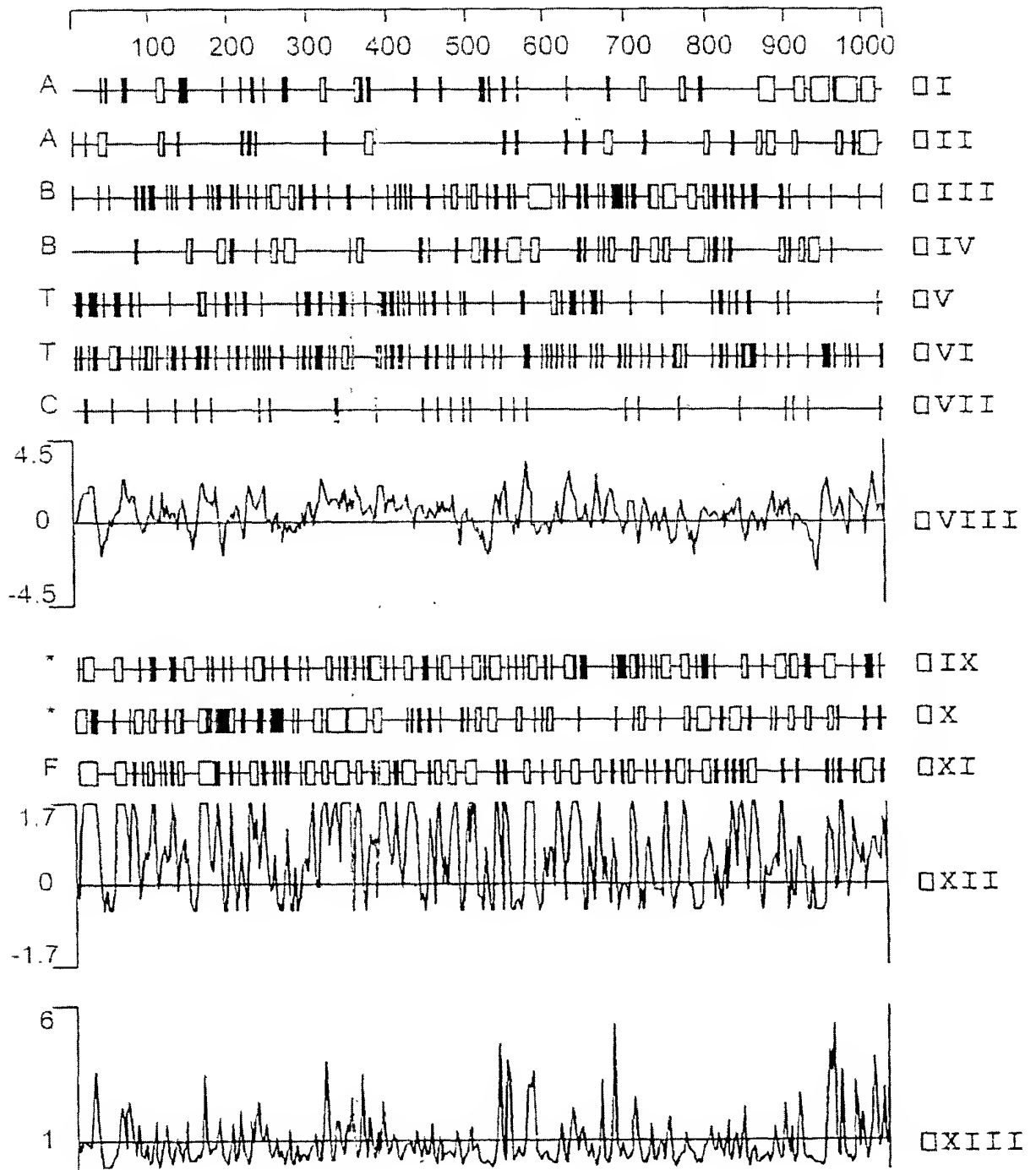
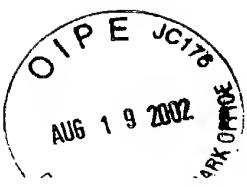


FIG. 5

	10	20	30	40	
1	M L F R A R G P V R G R G W G R P A E A P R R G R S P P W S P A W I C C W A L A	SEQ ID 2			
1	-----	SEC10			
	50	60	70	80	
41	G C Q A A W A G D L P S S S S R P L P P C Q E K D Y H F E Y T E C D S S G S R W	SEQ ID 2			
1	-----	SEC10			
	90	100	110	120	
91	R V A I P N S A V D C S G L P D P V R G K E C T F S C A S G E Y L E	SEQ ID 2			
1	-----	SEC10			
	130	140	150	160	
121	S K C G R G T Y S L G S G I K E D E W D E L P A G E S N I A T F M D T V V G P S	SEQ ID 2			
7	S K C G E G T Y S L G S G I K E D E W D E L P A G E S N I A T F M D T V V G P S	SEC10			
	170	180	190	200	
161	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G	SEQ ID 2			
47	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G	SEC10			
	210	220	230	240	
201	Y V F F E Y Q Y V D N N I F F E F F I O N D Q C Q E M D T T T D R W V K L T D N	SEQ ID 2			
87	Y V F F E Y Q Y V D N N I F F E F F I O N D Q C Q E M D T T T D R W V K L T D N	SEC10			
	250	260	270	280	
241	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A V K P V L V R N I T	SEQ ID 2			
127	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A V K P V L V R N I T	SEC10			
	290	300	310	320	
281	I E G V A Y T S E C F P C K R G T F S N K P G S F N C Q V C P R N T Y S E K G A	SEQ ID 2			
167	I E G V A Y T S E C F P C K R G T F S N K P G S F N C Q V C P R N T Y S E K G A	SEC10			
	330	340	350	360	
321	K E C I R C K D D S Q F S - - G S S E C T E R P P C T T R D Y F Q I H T P C D E	SEQ ID 2			
207	K E C I R C K D D S Q F S E E G S S E C T E R P P C T T R D Y F Q I H T P C D E	SEC10			
	370	380	390	400	
359	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K R D C P P C N F	SEQ ID 2			
247	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K R D C P P C N F	SEC10			
	410	420	430	440	
399	G F Y N N G S S S C H P C P F G T F S D G T K E C R P C P A G T E P A L G F E Y	SEQ ID 2			
287	G F Y N N G S S S C H P C P F G T F S D G T K E C R P C P A G T E P A L G F E Y	SEC10			
	450	460	470	480	
439	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G	SEQ ID 2			
327	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G	SEC10			
	490	500	510	520	
479	G S D N D Y L I L N L H I P G E K E P T S M T G A T G S E L G R I T F V F E T L	SEQ ID 2			
367	G S D N D Y L I L N L H I P G E K E P T S M T G A T G S E L G R I T F V F E T L	SEC10			

FIG. 6A



	530	540	550	560	
519	CSADCVLYFMVDINRRKSTNVVSWGGTKEKQAYTHLIPKN				SEQ ID 2
407	CSADCVLYFMVDINRRKSTNVVSWGGTKEKQAYTHLIPKN				SEC10
	570	580	590	600	
559	ATFTFTWAFQRRTNQGGQDNRRFINDMVKIYSITATNAVDGV				SEQ ID 2
447	ATFTFTWGIPIRE-----				SEC10
	610	620	630	640	
599	ASSCRACALGSEQSGSSCVPCPPGHYLEKETNQCKECPDP				SEQ ID 2
459	-----				SEC10
	650	660	670	680	
639	TYSIHQVYZGKEACIPCGPGSKNNQDHSVCYSDCFFYZHK				SEQ ID 2
459	-----				SEC10
	690	700	710	720	
679	ENQILHYDFSNLSSVGS LMN G E SFTSKGTYFHFNFISLC				SEQ ID 2
459	----- LIQ G E R				SEC10
	730	740	750	760	
719	GHEGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFVQCS				SEQ ID 2
464	-----				SEC10
	770	780	790	800	
759	TIIPSESKGFRAALSSQSIILADTFFIGVTVETTLKNINIK				SEQ ID 2
464	-----				SEC10
	810	820	830	840	
799	EDMFPPVPTSQIPDVHFFYKSSSTATTSCTINGRSTAVKMRCN				SEQ ID 2
464	-----				SEC10
	850	860	870	880	
839	PTKSGAGVISVPSKCPAGTCGCTFYFLWESAEACPLCTE				SEQ ID 2
464	-----				SEC10
	890	900	910	920	
879	HDFHEIEGACKRGFQETLYVWNEPKWCIGISLPEKKLAT				SEQ ID 2
464	-----				SEC10
	930	940	950	960	
919	CETVDFWLKVGAGVGAF TAVLLVALTCYFWKKKNQKKKKT I				SEQ ID 2
464	-----				SEC10
	970	980	990	1000	
959	LNLFN				SEQ ID 2
464	-----				SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 6B



	10	20	30	40	
1	M L F R A R G P V R G R G W G R P A Z A B R R G R S P P W S P A W I C C W A L A				SEQ ID 4
1	-----				SEC10
	50	60	70	80	
41	G C Q A A W A G D L P S S S S R P L P P C Q E K D Y A F E Y T E C D S S G S R W				SEQ ID 4
1	-----				SEC10
	90	100	110	120	
81	R V A I P N S A V D C S G L P D P V R G K E C T F S C A S G E Y L E				SEQ ID 4
1	-----				SEC10
	130	140	150	160	
121	S K C G E G T Y S L G S G I K F D E W D E L P A G E S N I A T F M D T V V G P S				SEQ ID 4
7	S K C G E G T Y S L G S G I K F D E W D E L P A G E S N I A T F M D T V V G P S				SEC10
	170	180	190	200	
161	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G				SEQ ID 4
47	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G				SEC10
	210	220	230	240	
201	Y V F F E Y Q Y V D N N I F F E F F I Q N D Q C Q E M D T T T D R W V K L T D N				SEQ ID 4
37	Y V F F E Y Q Y V D N N I F F E F F I Q N D Q C Q E M D T T T D R W V K L T D N				SEC10
	250	260	270	280	
241	G E W G S H S V M L R S G T N I L Y W R T T G I L M G S K A V K P V L V K N I T				SEQ ID 4
127	G E W G S H S V M L R S G T N I L Y W R T T G I L M G S K A V K P V L V K N I T				SEC10
	290	300	310	320	
281	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A				SEQ ID 4
167	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A				SEC10
	330	340	350	360	
321	K E C I R C K D D S Q F S - - G S S E C T E R F P C T T K D Y F Q I H T P C D E				SEQ ID 4
207	K E C I R C K D D S Q F S E E G S S E C T E R F P C T T K D Y F Q I H T P C D E				SEC10
	370	380	390	400	
359	E G K T Q I M Y R W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P				SEQ ID 4
247	E G K T Q I M Y R W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P				SEC10
	410	420	430	440	
399	G F Y N N G S S S C H F C P P G T F S D G T K E C R P C P A G T E P A L G F E Y				SEQ ID 4
287	G F Y N N G S S S C H F C P P G T F S D G T K E C R P C P A G T E P A L G F E Y				SEC10
	450	460	470	480	
439	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				SEQ ID 4
327	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				SEC10
	490	500	510	520	
479	G S D N D Y L I L N L E I P G F K P P T S M T G A T G S E L G R I T F V E E T L				SEQ ID 4
367	G S D N D Y L I L N L E I P G F K P P T S M T G A T G S E L G R I T F V E E T L				SEC10

FIG. 7A



519	CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHIEFN	SEQ ID 4
407	CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHIEFN	SEC10
559	ATETETWAFQR	SEQ ID 4
447	ATETETWGIPIRE	SEC10
599	ASSCRACALGSEQSGSSCVPCPPGHYIEKETNQCKECPD	SEQ ID 4
459	-----	SEC10
639	TYLSIHQVYGKEACIPCGPGSKNNQDHSVVCYSDCFFYHEK	SEQ ID 4
459	-----	SEC10
679	ENQILHYDFSNLSSVGS	SEQ ID 4
459	-----	SEC10
719	GHEGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFVCQS	SEQ ID 4
464	-----	SEC10
759	TIIPSESKGFRAALSSQSIILADTFIGVTVETTLKNINIK	SEQ ID 4
464	-----	SEC10
799	EDMEFPVPTSQIPDVHFFYKSSSTATTSCTINGRSTAVKMRCN	SEQ ID 4
464	-----	SEC10
839	PTKSGAGVISVPSKCPAGTCDGCTFYFLWESAEACPLCTE	SEQ ID 4
464	-----	SEC10
879	HDFHEIEGACKRGFQETLYVWNEPKWCICKISLPEKKLAT	SEQ ID 4
464	-----	SEC10
919	CETVDFWLKVGAGVGAFVALLVALTCYFWKKNQKLEYKY	SEQ ID 4
464	-----	SEC10
959	SKLVMTTNSKECELPAAADSCAIMEGEDNEEEVVYSNKQSL	SEQ ID 4
464	-----	SEC10
999	LGKLLSLATKEKEDHFEVQLKTSRSPNI	SEQ ID 4
464	-----	SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 7B

